



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number 10/786,445  
Source INFO  
Date Processed by STIC 3/8/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.

FOR CRF SUBMISSION AND PATENT IN SOFTWARE QUESTIONS, PLEASE CONTACT

MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22311-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Maltroun, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202.

Revised 10/08/03

**Raw Sequence Listing Error Summary**

<b>ERROR DETECTED</b>	<b>SUGGESTED CORRECTION</b>	<b>SERIAL NUMBER: 10/1786, 445</b>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS. (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present in <220>-<223> section, please explain location of n or Xaa, and which residue n or Xaa represents	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated in raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/786,445

DATE: 03/08/2004  
TIME: 15:16:40

Input Set : A:\Sequence Listing - Docket No. 096429-9141.txt  
Output Set: N:\CRF4\03082004\J786445.raw

3 <110> APPLICANT: Welch, Rodney A.  
4 Lathem, Wyndham W.  
5 Grys, Thomas E.  
7 <120> TITLE OF INVENTION: E. COLI O157:H7 C1-INH-BINDING PROTEIN AND METHODS OF USE  
9 <130> FILE REFERENCE: 096429-9141  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/786,445  
12 <141> CURRENT FILING DATE: 2004-02-25  
14 <150> PRIOR APPLICATION NUMBER: 10/002,309  
15 <151> PRIOR FILING DATE: 2001-10-26  
17 <150> PRIOR APPLICATION NUMBER: 60/243,675  
18 <151> PRIOR FILING DATE: 2000-10-26  
20 <160> NUMBER OF SEQ ID NOS: 25  
22 <170> SOFTWARE: PatentIn version 3.1  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 2798  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Unknown  
29 <220> FEATURE:  
30 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid  
p0157  
32 <220> FEATURE:  
33 <221> NAME/KEY: CDS  
34 <222> LOCATION: (138)..(2798)  
35 <223> OTHER INFORMATION:  
W--> 38 <400> 1

Does Not Comply  
Corrected Diskette Needed  
(Pg. 7)

39	tttacgaaac aggtgttaat atgttataaa aataacccaac gactagtcaa taatgtcgctc	60
41	ctgaaaaaat aaaaatataa aatactgtta tatccggctg catgaacact aaaaatgaatg	120
43	agatgtggag aacaccg atg aaaa tta aag tat ctg tca tgt acg atc ctt	170
44	Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu	
45	1 5 10	
47	gcc cct ctg gcg att ggg gta ttt tct gca aca gct gct gat aat aat	218
48	Ala Pro Leu Ala Ile Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn	
49	15 20 25	
51	tca gcc att tat ttc aat acc tcc cag cct ata aat gat ctg cag ggt	266
52	Ser Ala Ile Tyr Phe Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly	
53	30 35 40	
55	tcg ttg gcc gca gag gtg aaa ttt gca caa agc cag att tta ccc gcc	314
56	Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala	
57	45 50 55	
59	cat cct aaa gaa ggg gat agt cca cat ctg acc agc ctg cgg aaa	362
60	His Pro Lys Glu Gly Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys	
61	60 65 70 75	
63	agt ctg ctg ctt gtc cgt gtg aaaa gct gat gat aaaa aca cct gtt	410
64	Ser Leu Leu Leu Val Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val	

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Input Set : A:\Sequence Listing - Docket No. 096429-9141.txt  
Output Set: N:\CRF4\03082004\J786445.raw

65	80	85	90	
67	cag gtg gaa gcc cgc gat gat aat aat aaa att ctc ggt acg tta acc			458
68	Gln Val Glu Ala Arg Asp Asp Asn Lys Ile Leu Gly Thr Leu Thr			
69	95	100	105	
71	ctt tat cct cct tca tca cta ccg gat aca atc tac cat ctg gat ggt			506
72	Leu Tyr Pro Pro Ser Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly			
73	110	115	120	
75	gtt ccg gaa ggt ggt atc gat ttc aca cct cat aat gga acg aaa aag			554
76	Val Pro Glu Gly Gly Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys			
77	125	130	135	
79	atc att aat acg gtg gct gaa gta aac aaa ctc agt gat gcc agc ggg			602
80	Ile Ile Asn Thr Val Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly			
81	140	145	150	155
83	agt tct att cat acg cat cta aca aat aat gca ctg gtg gag atc cat			650
84	Ser Ser Ile His Ser His Leu Thr Asn Asn Ala Leu Val Glu Ile His			
85	160	165	170	
87	act gca aat ggt cgt tgg gta aga gac att tat ctg ccg cag gga ccc			698
88	Thr Ala Asn Gly Arg Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro			
89	175	180	185	
91	gac ctt gaa ggt aag atg gtt cgc ttt gtt tcg tct gca ggc tat agt			746
92	Asp Leu Glu Gly Lys Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser			
93	190	195	200	
95	tca acg gtt ttt tat ggt gat cga aaa gtc aca ctc tcg gtg ggt aac			794
96	Ser Thr Val Phe Tyr Gly Asp Arg Lys Val Thr Ser Val Gly Asn			
97	205	210	215	
99	act ctt ctg ttc aaa tat gta aat ggt cag tgg ttc cgc tcc ggt gaa			842
100	Thr Leu Leu Phe Lys Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu			
101	220	225	230	235
103	ctg gag aat aat cga atc act tat gct cag cat att tgg agt gct gaa			890
104	Leu Glu Asn Asn Arg Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu			
105	240	245	250	
107	ctg cct gcg cac tgg atc gtg cct ggt tta aac ttg gtg att aaa cag			938
108	Leu Pro Ala His Trp Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln			
109	255	260	265	
111	ggc aat ctg aca ggt cgc cta aat gat atc aag att gga gca ccg ggt			986
112	Gly Asn Leu Ser Gly Arg Ile Asn Asp Ile Lys Ile Gly Ala Pro Gly			
113	270	275	280	
115	gag ctg ttg ttg cat aca att gat atc ggg atg ttg acc act ccc cgg			1034
116	Glu Leu Leu His Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg			
117	285	290	295	
119	gat cgc ttt gat ttt gcc aaa gac aaa gaa gca cat agg gaa tat ttc			1082
120	Asp Arg Phe Asp Phe Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe			
121	300	305	310	315
123	cag acc att cct gta agt cgt atg att gtt aat aat tat gcg cct cta			1130
124	Gln Thr Ile Pro Val Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu			
125	320	325	330	
127	cac cta aag gaa gtt atg tta cca acc gga gag tta ttg aca gat atg			1178
128	His Leu Lys Glu Val Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met			
129	335	340	345	

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131	gat	cca	gga	aat	ggt	ggg	tgg	cat	agt	ggt	aca	atg	cgt	caa	aga	ata	1226
132	Asp	Pro	Gly	Asn	Gly	Gly	Trp	His	Ser	Gly	Thr	Met	Arg	Gln	Arg	Ile	
133				350					355							360	
135	ggt	aaa	gaa	tgg	ttt	tgc	cat	ggc	att	gat	aat	gct	aac	at	ggt	tta	1274
136	Gly	Lys	Glu	Leu	Val	Ser	His	Gly	Ile	Asp	Asn	Ala	Asn	Tyr	Gly	Leu	
137				365					370							375	
139	aat	agt	acc	gca	ggc	tta	ggg	gag	aat	agt	cat	cca	tat	gta	gtt	gcg	1322
140	Asn	Ser	Thr	Ala	Gly	Leu	Gly	Glu	Asn	Ser	His	Pro	Tyr	Val	Val	Ala	
141				380					385							390	395
143	caa	tta	ggc	gca	cat	at	agc	cgc	ggt	aat	tat	gct	aat	ggc	atc	cag	1370
144	Gln	Leu	Ala	Ala	His	Asn	Ser	Arg	Gly	Asn	Tyr	Ala	Asn	Gly	Ile	Gln	
145					400					405						410	
147	gtt	cat	ggc	ggc	tcc	gga	ggg	ggg	gta	att	gtt	act	tta	gat	tcc	aca	1418
148	Val	His	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ile	Val	Thr	Leu	Asp	Ser	Thr	
149					415					420						425	
151	ttg	ggg	aat	gag	tgc	agt	cat	gaa	gtt	ggg	cat	aat	tat	ggt	ctt	ggt	1466
152	Leu	Gly	Asn	Glu	Phe	Ser	His	Glu	Val	Gly	His	Asn	Tyr	Gly	Leu	Gly	
153					430					435						440	
155	cat	tat	gtt	aat	ggc	tgc	ggt	tcc	gta	cat	cgt	agt	gca	gaa	aat		1514
156	His	Tyr	Val	Asp	Gly	Phe	Lys	Gly	Ser	Val	His	Arg	Ser	Ala	Glu	Asn	
157					445					450						455	
159	aac	aac	tca	act	tgg	gga	tgg	gat	ggt	aat	aaa	aaa	cgg	ttt	att	cct	1562
160	Asn	Asn	Ser	Thr	Trp	Gly	Trp	Asp	Gly	Asp	Lys	Lys	Arg	Phe	Ile	Pro	
161					460					465						470	475
163	aac	ttt	tat	ccg	tct	caa	aca	aat	qaa	aag	agt	tgt	ctg	aat	aat	cag	1610
164	Asn	Phe	Tyr	Pro	Ser	Gln	Thr	Asn	Glu	Lys	Ser	Cys	Leu	Asn	Gln		
165						480				485						490	
167	tgt	caa	gaa	ccg	ttt	gat	gga	cac	aaa	ttt	ggt	ttt	gac	gcc	atg	gcg	1658
168	Cys	Gln	Glu	Pro	Phe	Asp	Gly	His	Lys	Phe	Gly	Phe	Asp	Ala	Met	Ala	
169						495					500					505	
171	gga	ggc	agc	cct	ttc	tct	gct	gca	aac	cgt	ttc	aca	atg	tat	act	ccg	1706
172	Gly	Gly	Ser	Pro	Phe	Ser	Ala	Ala	Asn	Arg	Phe	Thr	Met	Tyr	Thr	Pro	
173						510				515						520	
175	aat	tca	tgc	gtc	atc	atc	cag	cgt	ttt	ttt	gaa	aat	aaa	gct	gtg	tcc	1754
176	Asn	Ser	Ser	Ala	Ile	Ile	Gln	Arg	Phe	Phe	Glu	Asn	Lys	Ala	Val	Phe	
177							525				530					535	
179	gat	agc	cgt	tcc	tcc	acc	ggc	tcc	agc	aag	tgg	aat	gca	gat	acg	cag	1802
180	Asp	Ser	Arg	Ser	Ser	Thr	Gly	Phe	Ser	Lys	Trp	Asn	Ala	Asp	Thr	Gln	
181						540				545						550	555
183	gaa	atg	gaa	ccg	tat	gaa	cac	acc	att	gac	cgt	gcg	gag	cag	att	acg	1850
184	Glu	Met	Glu	Pro	Tyr	Glu	His	Thr	Ile	Asp	Arg	Ala	Glu	Gln	Ile	Thr	
185						560				565						570	
187	gct	tca	gtc	aat	gag	cta	agt	gaa	agc	aaa	atg	gct	gag	ctg	atg	gca	1898
188	Ala	Ser	Val	Asn	Glu	Leu	Ser	Glu	Ser	Lys	Met	Ala	Glu	Leu	Met	Ala	
189						575				580						585	
191	gag	tac	gtc	gtc	aaa	gtg	cat	atg	tgg	aac	ggt	aat	tgg	aca	aga		1946
192	Glu	Tyr	Ala	Val	Val	Lys	Val	His	Met	Trp	Asn	Gly	Asn	Trp	Thr	Arg	
193						590				595						600	
195	aac	atc	tat	atc	cct	aca	gcc	tcc	gca	aat	aga	ggc	agt	atc	ctg		1994

RAW SEQUENCE LISTING DATE: 03/08/2004  
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 Output Set: N:\CRF4\03082004\J786445.raw

196 Asn Ile Tyr Ile Pro Thr Ala Ser Ala Asp Asn Arg Gly Ser Ile Leu	
197 605 610 615	2042
199 acc atc aac cat gag ggc ggt tat aat aat gtc ttt ata aat ggt	
200 Thr Ile Asn His.Glu Ala Gly Tyr Asn Ser Tyr Leu Phe Asn Gly	
201 620 625 630 635	
203 gac gaa aag gtc gtt tcc cag ggg tat aat aag aac ttt gtt tcc gat	2090
204 Asp Glu Lys Val Val Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp	
205 640 645 650	
207 ggt cag ttc tgg aaa gaa cgt gat gtc gtt gat act cgt gaa gcg cgt	2138
208 Gly Gln Phe Trp Lys Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg	
209 655 660 665	
211 aag cca gag cag ttt ggt gtt cct gtc acc ctc gtc ggg tat tac	2186
212 Lys Pro Glu Gln Phe Val Pro Val Thr Thr Leu Val Gly Tyr Tyr	
213 670 675 680	
215 gat ccc gaa ggc acg ctc tca aac atc tat cct gcc atg tat ggt	2234
216 Asp Pro Glu Gly Thr Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly	
217 685 690 695	
219 gcc tat ggc ttc act tat tcc gat gat agt cag aat cta tcc gat aac	2282
220 Ala Tyr Gly Phe Thr Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn	
221 700 705 710 715	
223 gac tgc cag ctg cag gtc gat acg aaa gaa ggg cag ttg cga ttc aga	2330
224 Asp Cys Gln Leu Gln Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg	
225 720 725 730	
227 ctg gct aat cac cgg gct aac act gta atg aat aag ttc cat att	2378
228 Leu Ala Asn His Arg Ala Asn Asn Thr Val Met Asn Lys Phe His Ile	
229 735 740 745	
231 aac gtg cca aca gaa aat cag ccc aca cag gcc aca ttg gtt tgc aat	2426
232 Asn Val Pro Thr Glu Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn	
233 750 755 760	
235 aac aag ata ctg gat acc aaa tcg ctc aca cct gcg cca gaa gga ctt	2474
236 Asn Lys Ile Leu Asp Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu	
237 765 770 775	
239 acc tat act gta aat ggg cag gca ctt cca gca aaa gaa aac gag gga	2522
240 Thr Tyr Thr Val Asn Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly	
241 780 785 790 795	
243 tgc atc gtg tcc gtc gat aat tca ggt aaa cgt tac tgc ttg ccg gtt ggt	2570
244 Cys Ile Val Ser Val Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly	
245 800 805 810	
247 caa cgg tca gga tat aac ctt cct gac tgg att gtt ggg cag gaa gtc	2618
248 Gln Arg Ser Gly Tyr Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val	
249 815 820 825	
251 tat gtc gac agc ggg gct aaa gcg aaa gtc ctg ctt tct gac tgg gat	2666
252 Tyr Val Asp Ser Gly Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp	
253 830 835 840	
255 aac ctg tcc tat aac agg att ggt gag ttt gta ggt aat gtc aac cca	2714
256 Asn Leu Ser Tyr Asn Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro	
257 845 850 855	
259 gct gat atg aat aat ggt aat gcc tgg aac gga cag tat ttg gac ttc	2762
260 Ala Asp Met Lys Lys Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe	

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261 860 865 870 875  
 263 agt aaa cct agg tca atg agg gtt gta tat aaa taa 2798  
 264 Ser Lys Pro Arg Ser Met Arg Val Val Tyr Lys  
 265 880 885  
 268 <210> SEQ ID NO: 2  
 269 <211> LENGTH: 886  
 270 <212> TYPE: PRT  
 271 <213> ORGANISM: Unknown  
 273 <220> FEATURE:  
 274 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid  
 pO157  
 276 <400> SEQUENCE: 2  
 278 Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu Ala Pro Leu Ala Ile  
 279 1 5 10 15  
 282 Gly Val Phe Ser Ala Thr Ala Asp Asn Asn Ser Ala Ile Tyr Phe  
 283 20 25 30  
 286 Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly Ser Leu Ala Ala Glu  
 287 35 40 45  
 290 Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala His Pro Lys Glu Gly  
 291 50 55 60  
 294 Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys Ser Leu Leu Leu Val  
 295 65 70 75 80  
 298 Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val Gln Val Glu Ala Arg  
 299 85 90 95  
 302 Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr Leu Tyr Pro Pro Ser  
 303 100 105 110  
 306 Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly Val Pro Glu Gly Gly  
 307 115 120 125  
 310 Ile Asp Phe Thr Pro His Asn Gly Thr Lys Ile Ile Asn Thr Val  
 311 130 135 140  
 314 Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser  
 315 145 150 155 160  
 318 His Leu Thr Asn Asn Ala Leu Val Glu Ile His Thr Ala Asn Gly Arg  
 319 165 170 175  
 322 Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro Asp Leu Glu Gly Lys  
 323 180 185 190  
 326 Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser Ser Thr Val Phe Tyr  
 327 195 200 205  
 330 Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn Thr Leu Leu Phe Lys  
 331 210 215 220  
 334 Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu Leu Glu Asn Arg  
 335 225 230 235 240  
 338 Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu Leu Pro Ala His Trp  
 339 245 250 255  
 342 Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln Gly Asn Leu Ser Gly  
 343 260 265 270  
 346 Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly Glu Leu Leu His  
 347 275 280 285  
 350 Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg Asp Arg Phe Asp Phe  
 351 290 295 300

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/786,445

DATE: 03/08/2004

TIME: 15:16:41

Input Set : A:\Sequence Listing - Docket No. 096429-9141.txt

Output Set: N:\CRF4\03082004\J786445.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:38 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35  
L:658 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:655

<210> SEQ ID NO 4  
<211> LENGTH: 28  
<212> TYPE: DNA  
<213> ORGANISM Synthetic Oligonucleotide  
<400> SEQUENCE: 4  
ccctcgagtt tacgaaacag gtgttaat

(223)

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

Per new Sequence Rule(s),  
(213) response has to  
be either 28  
Artificial/Unknown  
or Genus/Species.  
please see  
item # 10  
on error  
summary  
sheet.